

RAW SEQUENCE LISTING

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Application Serial Number: 10/593,425
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/593,425

TIME: 14:48:25

Input Set : E:\13744- 21 US Sequence Listing.txt

Output Set: N:\CRF4\10102006\J593425.raw

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3 <110> APPLICANT: Feesche, Jorg
4     Meinhardt, Friedhelm
5     Nahrstedt, Hannes
6     Waldeck, Jens
7     Groene, Mark
8     Eichstadt, Renee
10 <120> TITLE OF INVENTION: Factor RecA From Bacillus Licheniformis and RecA-inactivated
11     Safety Stems Used for Biotechnological Production
13 <130> FILE REFERENCE: H 06291 (13744*21)
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/593,425
C--> 15 <141> CURRENT FILING DATE: 2006-09-19
15 <150> PRIOR APPLICATION NUMBER: PCT/EP05/001543
16 <151> PRIOR FILING DATE: 2005-02-16
18 <150> PRIOR APPLICATION NUMBER: DE 10 2004 013 988.1
19 <151> PRIOR FILING DATE: 2004-03-19
21 <160> NUMBER OF SEQ ID NOS: 32
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1047
27 <212> TYPE: DNA
28 <213> ORGANISM: Bacillus licheniformis DSM 13
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1047)
35 <220> FEATURE:
36 <221> NAME/KEY: gene
37 <222> LOCATION: (1)..(1047)
38 <223> OTHER INFORMATION: recA
41 <400> SEQUENCE: 1
42 atg agt gat cgt cag gca gcc tta gat atg gcg ctt aaa caa ata gaa      48
43 Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln Ile Glu
44 1             5             10             15
46 aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa act gaa      96
47 Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu
48             20             25             30
50 acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat gcg gct      144
51 Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
52             35             40             45
54 ctt gga gtg ggc gga tac ccg cgc ggc cgg att att gaa gta tac ggg      192
55 Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
56             50             55             60
58 cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att gcc gaa      240
59 Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu

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60	65					70						75					80		
62	gtt	cag	cag	cag	ggc	gga	caa	gcg	gcg	ttc	atc	gac	gcc	gac	acc	gcg		288	
63	Val	Gln	Gln	Gln	Gly	Gly	Gln	Ala	Ala	Phe	Ile	Asp	Ala	Asp	Thr	Ala			
64					85					90					95				
66	ctt	gat	ccc	gtc	tat	gca	caa	aag	ctg	ggc	gtc	aac	att	gat	gag	ctt		336	
67	Leu	Asp	Pro	Val	Tyr	Ala	Gln	Lys	Leu	Gly	Val	Asn	Ile	Asp	Glu	Leu			
68				100					105					110					
70	ttg	ctg	tca	cag	cct	gat	acg	ggc	gag	cag	gcg	ctc	gaa	atc	gct	gaa		384	
71	Leu	Leu	Ser	Gln	Pro	Asp	Thr	Gly	Glu	Gln	Ala	Leu	Glu	Ile	Ala	Glu			
72				115					120					125					
74	gcc	ctt	gtc	aga	agc	gga	gcg	gtg	gat	atc	gtt	gtc	atc	gac	tct	gta		432	
75	Ala	Leu	Val	Arg	Ser	Gly	Ala	Val	Asp	Ile	Val	Val	Ile	Asp	Ser	Val			
76		130				135						140							
78	gca	gcg	ctt	gtg	ccg	aaa	gct	gaa	atc	gaa	gga	gat	atg	ggg	gat	tcc		480	
79	Ala	Ala	Leu	Val	Pro	Lys	Ala	Glu	Ile	Glu	Gly	Asp	Met	Gly	Asp	Ser			
80	145				150					155				160					
82	cac	gtc	ggt	ttg	cag	gcc	aga	ctg	atg	tct	cag	gcg	ctt	cgc	aag	ctt		528	
83	His	Val	Gly	Leu	Gln	Ala	Arg	Leu	Met	Ser	Gln	Ala	Leu	Arg	Lys	Leu			
84				165					170					175					
86	tcc	gga	gcg	atc	aat	aaa	tcg	aag	acc	atc	gcg	atc	ttt	atc	aac	cag		576	
87	Ser	Gly	Ala	Ile	Asn	Lys	Ser	Lys	Thr	Ile	Ala	Ile	Phe	Ile	Asn	Gln			
88				180					185					190					
90	att	cgt	gaa	aaa	gtc	ggt	gtc	atg	ttt	gga	aat	cct	gag	acg	acg	cca		624	
91	Ile	Arg	Glu	Lys	Val	Gly	Val	Met	Phe	Gly	Asn	Pro	Glu	Thr	Thr	Pro			
92				195					200					205					
94	ggc	gga	aga	gcg	ctg	aaa	ttc	tac	tct	tct	gtc	cgc	ctt	gaa	gtg	cgc		672	
95	Gly	Gly	Arg	Ala	Leu	Lys	Phe	Tyr	Ser	Ser	Val	Arg	Leu	Glu	Val	Arg			
96		210				215						220							
98	cgc	gca	gag	cag	ctg	aaa	caa	ggc	aac	gac	gtc	atg	ggg	aac	aag	acg		720	
99	Arg	Ala	Glu	Gln	Leu	Lys	Gln	Gly	Asn	Asp	Val	Met	Gly	Asn	Lys	Thr			
100	225				230					235				240					
102	aaa	atc	aaa	gtc	gtg	aaa	aac	aaa	gtg	gca	cct	cca	ttc	cgg	aca	gcc		768	
103	Lys	Ile	Lys	Val	Val	Lys	Asn	Lys	Val	Ala	Pro	Pro	Phe	Arg	Thr	Ala			
104				245						250				255					
106	gaa	gtg	gac	att	atg	tac	ggg	gaa	gga	att	tca	aaa	gaa	ggg	gaa	atc		816	
107	Glu	Val	Asp	Ile	Met	Tyr	Gly	Glu	Gly	Ile	Ser	Lys	Glu	Gly	Glu	Ile			
108				260					265					270					
110	atc	gac	ctc	gga	aca	gag	ctt	gac	atc	gtt	caa	aag	agc	ggt	gca	tgg		864	
111	Ile	Asp	Leu	Gly	Thr	Glu	Leu	Asp	Ile	Val	Gln	Lys	Ser	Gly	Ala	Trp			
112				275					280					285					
114	tac	tct	tat	cag	gag	gaa	cgc	ctt	gga	caa	ggc	cgt	gaa	aac	gcc	aaa		912	
115	Tyr	Ser	Tyr	Gln	Glu	Glu	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Asn	Ala	Lys			
116		290				295						300							
118	cag	ttc	ctg	aaa	gaa	aac	aag	gat	atc	ctt	ttg	atg	att	caa	gag	cag		960	
119	Gln	Phe	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Leu	Met	Ile	Gln	Glu	Gln			
120	305				310					315				320					
122	atc	cgg	gag	cac	tac	ggt	ttg	gat	act	gga	ggc	gct	gct	cct	gca	cag		1008	
123	Ile	Arg	Glu	His	Tyr	Gly	Leu	Asp	Thr	Gly	Gly	Ala	Ala	Pro	Ala	Gln			
124				325						330				335					

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126 gaa gac gag gcc caa gct cag gaa gaa ctc gag ttt taa      1047
127 Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
128          340          345
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 348
133 <212> TYPE: PRT
134 <213> ORGANISM: Bacillus licheniformis DSM 13
136 <400> SEQUENCE: 2
138 Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln Ile Glu
139 1          5          10          15
142 Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu
143          20          25          30
146 Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
147          35          40          45
150 Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
151          50          55          60
154 Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu
155 65          70          75          80
158 Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala
159          85          90          95
162 Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu
163          100         105         110
166 Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu
167          115         120         125
170 Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val
171          130         135         140
174 Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser
175 145         150         155         160
178 His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu
179          165         170         175
182 Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln
183          180         185         190
186 Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro
187          195         200         205
190 Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg
191          210         215         220
194 Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr
195 225         230         235         240
198 Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala
199          245         250         255
202 Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile
203          260         265         270
206 Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp
207          275         280         285
210 Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys
211          290         295         300
214 Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln
215 305         310         315         320
218 Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln

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219                               325                               330                               335
222 Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
223                               340                               345
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 1792
228 <212> TYPE: DNA
229 <213> ORGANISM: Bacillus licheniformis
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (140)..(1336)
236 <220> FEATURE:
237 <221> NAME/KEY: gene
238 <222> LOCATION: (1)..(1792)
239 <223> OTHER INFORMATION: spoIV
242 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
244 <222> LOCATION: (140)..(142)
245 <223> OTHER INFORMATION: First codon translated as Met.
248 <400> SEQUENCE: 3
249 ggctgatgct caaacagggg cagtgcacatca ttcaaggcaa agactttgtc atcaaaacga      60
251 ttttgctga ggaaattctg cttgaaggca cgattgagct tgtccgctat atcgattcat      120
253 aagtcggggg gaaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga      172
254                               Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly
255                               1                               5                               10
257 aag atc cag ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat      220
258 Lys Ile Gln Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn
259                               15                               20                               25
261 gaa tgc acc agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa      268
262 Glu Cys Thr Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys
263                               30                               35                               40
265 gac gcc gtc ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg      316
266 Asp Ala Val Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg
267                               45                               50                               55
269 aag gtc atc aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa      364
270 Lys Val Ile Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys
271 60                               65                               70                               75
273 ggg ttt cct ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act      412
274 Gly Phe Pro Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr
275                               80                               85                               90
277 ttt gga gtt gct gca ttt ttt atc atc atg ctc cta ttg tcc aac atg      460
278 Phe Gly Val Ala Ala Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met
279                               95                               100                               105
281 ctt tgg aaa att gat att aca gga gcc aat ccg gag aca gaa cat caa      508
282 Leu Trp Lys Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln
283                               110                               115                               120
285 atc aaa cag caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag      556
286 Ile Lys Gln Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln
287                               125                               130                               135
289 ttt tca atg ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg      604

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290	Phe	Ser	Met	Leu	Thr	Pro	Glu	Lys	Ile	Gln	Gln	Ala	Leu	Thr	Lys	Arg	
291	140					145				150						155	
293	gtc	gaa	aac	atc	act	tgg	gtg	ggt	att	gag	tta	aac	ggc	acc	gcc	ctt	652
294	Val	Glu	Asn	Ile	Thr	Trp	Val	Gly	Ile	Glu	Leu	Asn	Gly	Thr	Ala	Leu	
295				160						165					170		
297	cac	atg	aaa	gtc	ggt	gaa	aag	aat	gaa	cct	gac	aaa	gaa	aaa	tat	atc	700
298	His	Met	Lys	Val	Val	Glu	Lys	Asn	Glu	Pro	Asp	Lys	Glu	Lys	Tyr	Ile	
299				175					180						185		
301	ggt	ccg	agg	cac	atc	gtc	gcc	aaa	aaa	ggg	gcg	acc	atc	tcg	aaa	aag	748
302	Gly	Pro	Arg	His	Ile	Val	Ala	Lys	Lys	Gly	Ala	Thr	Ile	Ser	Lys	Lys	
303			190						195					200			
305	ttc	gtg	gaa	aaa	ggc	gag	ccg	ctc	gtc	acg	gtg	aac	cag	cac	gtt	gaa	796
306	Phe	Val	Glu	Lys	Gly	Glu	Pro	Leu	Val	Thr	Val	Asn	Gln	His	Val	Glu	
307		205					210					215					
309	aaa	ggg	caa	atg	ctc	ggt	tcc	ggg	ctg	atc	gga	agc	gaa	gag	gaa	aag	844
310	Lys	Gly	Gln	Met	Leu	Val	Ser	Gly	Leu	Ile	Gly	Ser	Glu	Glu	Glu	Lys	
311	220					225					230				235		
313	caa	aaa	gtc	gga	gca	aaa	ggg	aaa	atc	tac	ggt	gaa	acc	tgg	tac	aag	892
314	Gln	Lys	Val	Gly	Ala	Lys	Gly	Lys	Ile	Tyr	Gly	Glu	Thr	Trp	Tyr	Lys	
315				240						245					250		
317	tca	aca	gta	acg	ggt	cct	ctt	gag	aca	tca	ttt	gac	ggt	ttt	acg	ggt	940
318	Ser	Thr	Val	Thr	Val	Pro	Leu	Glu	Thr	Ser	Phe	Asp	Val	Phe	Thr	Gly	
319				255					260					265			
321	aaa	gta	agg	aca	agt	cac	aag	cta	tcc	ctc	gga	tca	ttt	tcc	gtg	ccg	988
322	Lys	Val	Arg	Thr	Ser	His	Lys	Leu	Ser	Leu	Gly	Ser	Phe	Ser	Val	Pro	
323			270						275					280			
325	atc	tgg	ggc	ttt	tca	ttt	aaa	aaa	gaa	gac	ttc	tcg	cgc	ccg	aag	acg	1036
326	Ile	Trp	Gly	Phe	Ser	Phe	Lys	Lys	Glu	Asp	Phe	Ser	Arg	Pro	Lys	Thr	
327		285					290					295					
329	gag	acc	gaa	aac	ccc	tcg	ctg	cat	ttt	atg	aat	ttt	aag	ctt	cct	gtc	1084
330	Glu	Thr	Glu	Asn	Pro	Ser	Leu	His	Phe	Met	Asn	Phe	Lys	Leu	Pro	Val	
331	300					305					310				315		
333	gct	tat	gaa	aag	gag	cat	atg	agg	gag	agc	gaa	caa	atc	aaa	agg	gtg	1132
334	Ala	Tyr	Glu	Lys	Glu	His	Met	Arg	Glu	Ser	Glu	Gln	Ile	Lys	Arg	Val	
335				320						325					330		
337	tac	tcg	aaa	aaa	gaa	gca	ggt	ctt	gaa	gga	atc	gaa	atg	gga	aaa	aga	1180
338	Tyr	Ser	Lys	Lys	Glu	Ala	Val	Leu	Glu	Gly	Ile	Glu	Met	Gly	Lys	Arg	
339				335					340					345			
341	gac	atc	agg	aaa	aaa	atc	ggc	agc	gac	ggg	aac	att	atc	agt	gaa	aaa	1228
342	Asp	Ile	Arg	Lys	Lys	Ile	Gly	Ser	Asp	Gly	Asn	Ile	Ile	Ser	Glu	Lys	
343			350				355					360					
345	ggt	ttg	cac	gaa	acg	agc	gag	aat	ggc	aaa	ggt	aaa	ttg	atc	atc	ctt	1276
346	Val	Leu	His	Glu	Thr	Ser	Glu	Asn	Gly	Lys	Val	Lys	Leu	Ile	Ile	Leu	
347		365					370					375					
349	tac	cag	ggt	att	gaa	gac	att	ggt	caa	aca	aca	cca	att	ggt	cag	gag	1324
350	Tyr	Gln	Val	Ile	Glu	Asp	Ile	Val	Gln	Thr	Thr	Pro	Ile	Val	Gln	Glu	
351	380					385					390				395		
353	act	aaa	gaa	tga	cagaacactt	acttgcaatt	catcagcaac	tggaaagtcc									1376
354	Thr	Lys	Glu														

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date